

Db	96	tppappedprggagnasrdgrpsgggrpprpkappkerkw	140	
Qy	274	SPARAEATSLLEGALSGTRSHPSVGROHAPPSTSRP-PRPW	317	
RESULT	2	standard; Protein: 402 AA.		
ID	W36855;			
AC	W36855;			
DT	10-MAR-1998	(first entry)		
DE	Full length sequence of human osteogenic protein 2 (hop-2).			
KW	Human osteogenic protein; OP; OP-2; morphogen; morphogenic protein;			
KW	embryogenesis; organ maintenance; tissue-specific morphogenesis;			
KW	arthritis; emphysema; osteoporosis; cirrhosis.			
OS	Homo sapiens.			
FT	Location/Qualifiers			
FT	18..263			
FT	/note= "pro region which is cleaved to yield the mature morphogenically active protein"			
Protein	264..402			
Region	/note= "mature protein"			
FT	301..402			
FT	/note= "conserved 7 Cys skeleton"			
PN	US5650276-A.			
PD	22-JUL-1997.			
PF	20-JUL-1994; 278729.			
PR	28-AUG-1993; US-938021.			
PR	30-AUG-1991; US-752661.			
PR	30-AUG-1991; US-752861.			
PA	(CREA-) CREATIVE BIOMOLECULES INC.			
CC	Cohen CM, Kuberanpath T, Oppermann H, Ozkaynak E;			
CC	Pang RH, Rueger DC, Smart JE;			
WPI	97-384655/35.			
DR	NP-PSDB; T97881.			
DR	Screening for compounds which modulate morphogen expression - by incubating in the presence of epithelial cells which contain a cellular gene for morphogenically active protein expression			
PS	Disclosure: Columns 61-64; 49pp; English.			
CC	The present sequence represents a human osteogenic protein-2 (hop-2).			
CC	Op-2 proteins are a group of morphogenically active proteins. Morphogens are inactive when reduced, but are active as oxidised homodimers and when oxidised with other morphogens (e.g. W3655-62). Comparison of the amino acid sequences of these morphogens has identified a consensus 6-7 cysteine motif at the C-terminal. Morphogenic proteins such as op-2 play an important role, not only in embryogenesis, but also in tissue and organ maintenance, and repair in mammals. They induce a developmental cascade of tissue-specific morphogenesis in a mammal. A novel method is described for screening a candidate compound for the ability to modulate expression of a cellular gene encoding a naturally occurring morphogenic protein. The candidate compound is incubated with epithelial cells which express the cellular gene, and after a period of time the epithelial cells are assayed for the presence of or the amount of the protein expressed by the cellular gene. A change in the level of the morphogenic protein relative to the level in the epithelial cells in the absence of the candidate compound is indicative of the ability of the compound to modulate expression of the cellular gene. The method can be used to identify compounds which can increase or decrease morphogen production or levels. Such compounds can be used in the treatment of, e.g. arthritis, emphysema, osteoporosis, kidney disease, lung diseases, cardiologyopathy, and cirrhosis of the liver.			
CC	Sequence 402 AA;			
RESULT	3	standard; Protein: 402 AA.		
ID	R50238			
AC	R50238			
DT	11-OCT-1994	(first entry)		
DE	Human OP-2.			
KW	OP-1; OP-2; CBMP2; Vg1(fx); Vgr(fx); DPP(fx); BMP6(fx);			
KW	GDP-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP6(fx);			
KW	osteogenic protein; morphogen; morphogenic protein; liver; regeneration; injury; cancer; integration; transplant; gene therapy; hepatic tissue.			
KW	Homo sapiens			
PN	W0406449-A.			
PD	31-MAR-1994.			
PR	16-SEP-1992; US-046238.			
PR	16-SEP-1992; US-029335.			
PR	04-MAR-1993; US-029335.			
PA	31-MAR-1993; US-040510.			
PA	(CREA-) CREATIVE BIOMOLECULES INC.			
PI	Cohen CM, Kuberanpath T, Oppermann H, Ozkaynak E;			
PI	Pang RH, Rueger DC, Smart JE;			
DR	WPI: 94-118148/14.			
DR	N-PSDB; Q45144.			
PT	Use of morphogen(s) to induce liver regeneration - for repair of injury, treatment of cancer etc., also to improved integration of transplant tissue, in gene therapy etc.			
PT	Claim 42-42; Page 134-136; 176pp; English.			
PS	Morphogens comprising an amino acid sequence sharing at least 70% homology with OP-1, OP-2, CBMP2, Vg1(fx), Vgr(fx), GDP-1(fx), 60A(fx) are useful for maintaining liver function in a mammal, including means for regenerating lost or damaged hepatic tissue, means for enhancing viability and integration of hepatic tissue, and organ transplants, and means for correcting liver function deficiencies, including means for enhancing diminished liver function due to tissue injury or disease.			
CC	Use of BMP3(fx), BMP5(fx) and BMP6(fx) are included in the disclosure 402 AA;			
SQ	Query Match Score 125; DB 10; Length 402; Best Local Similarity 39.7%; Pred. No. 1.45e+00; Mismatches 21; Indels 5; Gaps 5; Matches 25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;			
Db	12 gialcalggggpglrrppp-gc-pqrllg-arerrdvqreilavlgplgr-prrppaas 67			
Qy	172 GPPLYQLGAAQTQA-RPPPHASGPRLGGERAWNHSSVREGVPLGLPAPGARRGGGSASR 230			
Db	68 rlp 70			
Qy	231 SLP 233			
RESULT	4	standard; Protein: 402 AA.		
ID	R51937			
AC	R51937;			
DT	15-OCT-1994	(first entry)		
DE	Osteogenic protein hop2-PP.			
KW	Morphogenic protein; hop2-PP; OP-2; hop2; hop-2; tissue morphogenesis; osteogenic protein.			
KW	Homo sapiens			
OS	W0410263-A.			
PN	W0410263-A.			
PD	11-MAY-1994.			
PF	02-NOV-1992; US-971091.			
PR	03-NOV-1992; US-971091.			
PR	04-MAR-1993; US-040510.			
PA	(CREA-) CREATIVE BIOMOLECULES INC.			
PI	Cohen CM, Kuberanpath T, Oppermann H, Ozkaynak E;			
PI	Pang RH, Rueger DC;			
DR	WPI: 94-167312/20.			
DR	N-PSDB; Q55935.			
PT	A morphogenically active protein MOP-3 - for inducing tissue			

PT morphogenesis in mammals
 PS Disclosure; Page 125-131; 164pp; English.
 CC A novel mouse morphogenic protein, OP3, has the sequence given in
 CC R54934, and is encoded by cDNA of sequence Q65390. cDNA and protein
 CC sequences were also provided for human osteogenic protein OP1
 CC (Q65391, R54935), mouse OP1 (Q65392, R54936), human OP2 (Q65393,
 CC R54937) and mouse OP2 (Q65394, R54938) as well as the genomic DNA
 CC sequence of human OP2 (Q65395). Generic sequences given in R54939-
 CC 40 accomodate homologies between OP1, OP2, OP3 and other morphogen
 CC protein family members.
 Sequence 402 AA;
 SQ

Query	Match	1.5%	Score 125; DB 10; Length 402;
Best Local Matches	Similarity 39.7%; Conservative 25;	Pred. No. 1.45e+00; Mismatches 12; Mismatches 21;	Indels 5; Gaps
Db	12 glalalggggplrrpp-gc-parrgg-aerrrdqgrllavlgplgr-prppaaaa 67		
Qy	172 GPPLVQLGATQA-RPPPHASGPRRLGCERAWNHSYREAGVPLGLPAPGARRRGGSR 230		
	68 rlp 70		
	231 SLP 233		

RESULT 5 R60578 standard; Protein; 402 AA.
 ID R60578;
 AC R60578;
 DT 30-MAR-1995 (first entry)
 DE Osteogenic protein OP2.
 KW Osteogenic protein.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cleavage_site 239..242 /note= "proteolytic cleavage site"
 FT cleavage_site 260..263 /note= "proteolytic cleavage site"
 FT PN W09420539 A.
 PD 15-SEP-1994.
 PF 04-MAR-1994; U02335
 PR 04-MAR-1993; US-02/070.
 PA (CREA-) CREATIVE BIOMOLECULES INC.
 PI Jones WK, Oppermann H, Ozkaynak E, Rueger DC,
 Tucker RF, Sampath KT;
 PI WPI: 94-302971/37.
 DR P-PSDB; Q71426.
 DR Binding Partners, esp. antibodies, specific for different forms
 PT of osteogenic protein - for differentiating between mature and
 PT soluble complexed forms of the protein in culture media or serum.
 Disclosure: Page 50-52; 70pp; English.
 CC The osteogenic protein is produced recombinantly in mammalian cell
 CC cultures, and may be provided to a site for bone induction in a
 CC mammal with a suitable matrix to allow infiltration and proliferation
 CC and differentiation of migrating progenitor cells.
 CC

Length 482;
BB 113;
Score 125;

	Matches	25;	Conservative	12;	Mismatches	21;	Indels	5;	Gaps	
Db	12	gla	al	gggg	g	lrrppp	gc-parrly	-aerr	rrdqvqslavlglpgr-prbrappaas	67

QY 172 GPLYOLGAATQA-RRPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGARRGGSASR 230

Db 68 rlp 70
||

RESULT ⁶
 ID R57973 standard; Protein: 402 AA.
 AC R57973;
 DT 11-OCT-1994 (first entry)

DE	Human OP-2.
KW	OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); DPP(fx);
KW	GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP6(fx);
KW	tooth socket; alveolus; osteogenic protein; morphogen;
KW	morphogenic protein; periodontal tissue; regeneration;
KW	tooth implant; integration; inhibition.
OS	Homo sapiens.
PN	WO9406399-A.
PD	31-MAR-1994.
PF	15-SEP-1993; US08742.
PR	15-SEP-1992; US 94 5285.

PR 04-APR-1993 - US-040510.
PA (CREA) CREATIVE BIOMOLECULES INC.
PI Cohen CM, Kubera-Sampath T, Oppermann H, Ozkaynak E;
Pang RHL, Rueger DC, Smart JE;
WI; 94-11810/7-14.
DR N/PDSB: 067313.

PT Morphogen-induced periodontal tissue regeneration - use of
PT integrating as implanted tooth in tooth socket or to in-
PT tissue loss associated with periodontal disease or inju-
PS Claim 28-29; Page 96-98.
CC Morpheus Comprising an amino acid sequence sharing at

	Query Match	Match	Score	Length
CC	homology with OP-1, OP-2, CBMP2, Vgr(fx), GDF-1(fx), BMP5(fx) and at least 80% homology with BMP6(fx)	Vgr(fx), GDF-1(fx), BMP5(fx) and BMP6(fx)	1.58	402 AA;
CC	tooth in a tooth socket and for inhibiting tissue loss with periodontal disease or injury.		39.78	
SQ	Sequence		39.78	
Db	glialcalggggg1rppp-gc-pqrirg-arerrdvqrelav1q1pgr	12	125	DB 9; Length 4
Db	: : : : : : : : : : : :	25	1.45e+00;	Pred. No. 12; Mismatches 21; Index 21;
Db	rplp 70	172	1.45e+00;	Mismatches 21; Index 21;
Qy	GGPLYOLQAA1QA-RPPPHASGPRRRLGCBRAWNHSVREAGVPLGLPAPG	231	1.45e+00;	
Db	SLP 233		1.45e+00;	
Qy			1.45e+00;	
RESULT				
ID	R27291	standard	402 AA.	7
AC	R27291;			
DT	26-FEB-1993	(first entry)		
DE	Human osteogenic protein hop2.			
KW	Morphogenic protein.			
OS	Homo sapiens.			
PN	W0921333-A.			
PD	17-SEP-1992.			
PF	11-MAR-1992;	001968.		
PR	11-MAR-1991;	US-567274.		

PI Cohen CM, Kuberasampath T, Oppermann H, Pang RHL, Rueger DC;
WPA; 92-3145/40.

DR N/PDB; Q2873.

PT Compsns. for increasing progenitor cell population I contain
morphogen to induce proliferation, useful for inhibiting
neoplastic growth, inducing tissue repair and in diagnosis of
tissue dysfunction

PT Disclosure; Page 93-95; 132PP; English.

CC Mature hop2 is one of the preferred known morphogens which can
be used in the manufacture of pharmaceuticals for inducing non-
chondrogenic mammalian tissue growth, progenitor cell prolifc
and hepatic tissue growth and for maintaining the phenotypic
expression of differentiated cells in a mammal. Morphogenic
compositions of the invention can also be used to treat bloo
disorders and impaired or lost immune function. Morphogens sh
at least 70% homology with hop2 are included.

SQ Sequence 402 AA;

PT endochondral bone formation when in association with a matrix
 PS Claim 26; Columns 143-148; 128pp; English.
 CC The osteogenic protein when in association with a matrix can induce
 at the locus of an implant the full development cascade of
 endochondral bone formation including vascularisation,
 mineralisation and bone marrow differentiation. The osteogenic
 protein can also be used to repair both bone and cartilage in the
 treatment of osteoarthritis. This is the pre-pro form of the
 protein.

SQ Sequence 402 AA;

Query Match 1.5%; Score 125; DB 8; Length 402;
 Best Local Similarity 39.7%; Pred. No. 1.4e+00;

Matches 25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;

Db 12 glalcalggggpgrlrrppp-gc-pqrllg-acerrdvrellavlgplgr-prprappaas 67
 Qy 172 GPPLYQLGAAATQA-RPPHASGPRRLGCERAWNHSVREAGYPLGLPAPGARRGGSASR 230

Db 68 rlp 70
 FT 11
 FT 231 SLP 233

RESULT 11
 ID R33410 standard; Protein: 402 AA.
 AC R33410;

ID Human OP-2-PP; 15-JUL-1993 (first entry)
 DE Human OP-2-PP.
 KW morphogenic; osteogenic protein; developmental cascade; hop-2;
 inflammation; anti-inflammatory; Transforming Growth Factor;
 KW TGF-beta super-familly; hippocampus;
 OS Homo sapiens.
 Key Cohen CM, Kubarsampath T, Oppermann H, Ozkaynak E;
 PANG RHL, Rueger DC, Smart JE;
 WPI: 93-100652/12.

DR N-PSDB, Q38735.
 PT Morphogen-induced modulation of inflammatory response - and
 resulting tissue damage, e.g. in autoimmune diseases, diabetes,
 asthma, ischemia, reperfusion injury, etc.
 CLaim 26; Page 121-123; 16pp; English.

CC Human osteogenic protein (OP)-2 is a preferred morphogen for use in
 treating tissue damage in e.g. inflammatory disease, autoimmune
 disease, arthritis, psoriasis, dermatitis, diabetes and emphysema.
 Proteins having at least 70% homology with OP-2 amino acid
 sequences can also be used. See R33400 for mature hop-2.

SQ Sequence 402 AA;

Query Match 1.5%; Score 125; DB 6; Length 402;
 Best Local Similarity 39.7%; Pred. No. 1.4e+00;

Matches 25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;

Db 12 glalcalggggpgrlrrppp-gc-pqrllg-acerrdvrellavlgplgr-prprappaas 67
 Qy 172 GPPLYQLGAAATQA-RPPHASGPRRLGCERAWNHSVREAGYPLGLPAPGARRGGSASR 230

Db 68 rlp 70
 FT 11
 FT 231 SLP 233

AC W00238;	DT 21-NOV-1996 (first entry)
DE Human osteogenic protein OP-2.	KW Morphogen; osteogenic protein; dentine; tooth decay; caries;
OS Homo sapiens.	KW morphogenesis; odontoblast; OP-2.
Key	Location/Qualifiers
FT peptide	1..17
FT region	/label= sig-peptide
FT region	18..263
FT protein	/label= Pro_region
FT domain	264..402
FT domain	/label= Mat_protein
FT domain	301..402
FT domain	/label= 7-Cys_C-terminal_domain
PN W0926777-61.	PR 01-MAR-1995; US-3196930.
PD 06-SEP-1996.	PA (CREA-) CREATIVE BIOMOLECULES INC.
PF 14-FEB-1996.	PI Charette MF, Ruthard RB;
WPI: 96-412583/41.	DR WPI; 96-412583/41.
DR N-PSDB; T33443.	DR N-PSDB; T33443.
PT Use of morphogen(s), e.g. osteogenic proteins, on dentinal surfaces	PT Use of morphogen(s), e.g. osteogenic proteins, on dentinal surfaces
PS Disclosure; Page 58-59; 106pp; English.	PT - for inducing dentine morphogenesis, desensitising teeth or sealing
PT tooth cavities	PT tooth cavities
PS Disclosure; Page 58-59; 106pp; English.	PS Disclosure; Page 58-59; 106pp; English.
CC Human hippocampus full-length osteogenic protein OP-2 (W00238)	CC Human hippocampus full-length osteogenic protein OP-2 (W00238)
CC includes a pro-sequence and the morphogenically active mature	CC includes a pro-sequence and the morphogenically active mature
CC protein sequence (see also W00223) that includes a 7-Cys C-terminal	CC protein sequence (see also W00223) that includes a 7-Cys C-terminal
CC domain. OP-2 can be expressed from intact or truncated cDNA	CC domain. OP-2 can be expressed from intact or truncated cDNA
CC (T33443) in prokaryotic or eukaryotic host cells. Mature OP-2 and	CC (T33443) in prokaryotic or eukaryotic host cells. Mature OP-2 and
CC other morphogens (see also W00221-35). Paric. human OP-1 (W00221).	CC other morphogens (see also W00221-35). Paric. human OP-1 (W00221).
CC can be used to induce dentine morphogenesis to seal dental cavities	CC can be used to induce dentine morphogenesis to seal dental cavities
CC and to desensitise teeth to pressure and/or temp.	CC and to desensitise teeth to pressure and/or temp.
SQ Sequence 402 AA;	SQ Sequence 402 AA;
Query Match 1.5%; Score 125; DB 19; Length 402;	Query Match 1.5%; Score 125; DB 19; Length 402;
Best Local Similarity 39.7%; Pred. No. 1.45e100;	Best Local Similarity 39.7%; Pred. No. 1.45e100;
Matches 25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;	Matches 25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;
Db 12 glalcalggggpgrlrrppp-gc-pqrllg-acerrdvrellavlgplgr-prprappaas 67	Db 12 glalcalggggpgrlrrppp-gc-pqrllg-acerrdvrellavlgplgr-prprappaas 67
Qy 172 GPPLYQLGAAATQA-RPPHASGPRRLGCERAWNHSVREAGYPLGLPAPGARRGGSASR 230	Qy 172 GPPLYQLGAAATQA-RPPHASGPRRLGCERAWNHSVREAGYPLGLPAPGARRGGSASR 230
Db 68 rlp 70	Db 68 rlp 70
FT 11	FT 11
FT 231 SLP 233	FT 231 SLP 233
RESULT 13	RESULT 13
ID R47292 standard; Protein: 402 AA.	ID R47292 standard; Protein: 402 AA.
AC R47292;	AC R47292;
DT 02-SEP-1994 (first entry)	DT 02-SEP-1994 (first entry)
DE hop2.	DE hop2.
Human; hippocampus; osteogenic protein; OP-1; hop-1; mature; injury;	Human; hippocampus; osteogenic protein; OP-1; hop-1; mature; injury;
KW survival; neural cell; morphogen; chemical; mechanical; neuropathy;	KW survival; neural cell; morphogen; chemical; mechanical; neuropathy;
KW transected nerves; demyelinated cell; toxin; ethanol; Parkinson's;	KW transected nerves; demyelinated cell; toxin; ethanol; Parkinson's;
KW Alzheimers; Huntington's chorea; amyotrophic lateral sclerosis;	KW Alzheimers; Huntington's chorea; amyotrophic lateral sclerosis;
KW multiple sclerosis; neoplastic lesion; central nervous system; CNS;	KW multiple sclerosis; neoplastic lesion; central nervous system; CNS;
KW retinoblastoma; glial cell neoplasm; redifferentiation; neuroblastoma;	KW retinoblastoma; glial cell neoplasm; redifferentiation; neuroblastoma;
KW peripheral nervous system; neurite; outgrowth; cell aggregation;	KW peripheral nervous system; neurite; outgrowth; cell aggregation;
KW cell adhesion; axonal; nerve regeneration; vascularisation;	KW cell adhesion; axonal; nerve regeneration; vascularisation;
KW myelin sheath.	KW myelin sheath.
OS Homo sapiens.	OS Homo sapiens.
PN W09403200-A.	PN W09403200-A.
PD 17-FEB-1994.	PD 17-FEB-1994.
PF 29-JUL-1993; U07189.	PF 29-JUL-1993; U07189.
PR 31-JUL-1992; US-932813.	PR 31-JUL-1992; US-932813.
PR 04-MAR-1993; US-039335.	PR 04-MAR-1993; US-039335.
PR 31-MAR-1993; US-040510.	PR 31-MAR-1993; US-040510.
PA (CREA-) CREATIVE BIOMOLECULES INC.	PA (CREA-) CREATIVE BIOMOLECULES INC.
PI Jones WK, KuberaSampath T, Oppermann H, Ozkaynak E;	PI Jones WK, KuberaSampath T, Oppermann H, Ozkaynak E;

RESULT 12
 ID W00238 standard; Protein: 402 AA.

Jones WK, KuberaSampath T, Oppermann H, Ozkaynak E;

Rueger DC, Tucker RF;
WPI: 94-065399/08.
N-PSDB; Q56233.

Use morphogens to improve survival of neural cells - also stimulating re-differentiation in transformed cells and prodn. of adhesion molecules, for treating traumatic injury, neuropathy and nerve cell cancers, etc.

Claim 23, Page 131-134; 176pp; English.

This sequence represents the human hippocampus derived protein, osteogenic protein, hop-2. The mature OP-1 protein was used in the method of the invention for improving survival of neural cells. Morphogens such as this, can be used to treat (protect) cells which have suffered chemical or mechanical injury, eg. transected nerves; demyelinated cells; cells exposed to toxins such as ethanol, and cells at risk because of neuropathies (such as Parkinsons and Alzheimers diseases; Huntingtons chorea; amyotrophic lateral sclerosis or multiple sclerosis), or because of neoplastic lesions (esp. retinoblastoma or glial cell neoplasms). At risk cells can be in the central or peripheral nervous systems. When used to induce redifferentiation, morphogens such as this, are used to treat neuroblastoma and then induce formation of neurite outgrowths, cell aggregation and/or cell adhesion. These proteins stimulate complete axonal nerve regeneration, including vascularisation and reformation of the myelin sheath. Nerves can be regenerated over long distances, eg. greater than 10mm.

	Matches	25:	Conservative	12:	Mismatches	21:	Indels	5:	Gaps	5:
Db	12	g	alcalggggpplroppp-gc-pqrllg-arerrdqvrellavlg1pgr-prprappaas							67
Qy	172	GPPPLYOLGAATQA-RPPPHASSGPRRLGCERAWNHSVREAGVPLGPAPGARRGGSASR								230
Db	68	r1P	70							
Qy	231	SLP	233							

Search completed: Thu Jul 30 14:44:41 1998
Job time : 102 secs.

Db 143 PPPPGGGOPRPPGPPPTGPQPRPTOGP-PP 172
 : | : | :: |||: ||| : | |
 Qy 295 SHPSVGHQHAA-GPPSISRPPAPWDPICPP 323

RESULT 7 S16681 #type complete
 ENTRY homoeotic protein - human
 TITLE #formal_name Homo sapiens #common_name man
 ORGANISM 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
 DATE 17-Oct-1997
 ACCESSIONS S16681
 REFERENCE Deguchi, Y.; Kehrl, J.H.
 #authors Nucleic Acids Res. (1991) 19:3742
 #journal Nucleotide sequence of a novel diverged human homeobox gene
 #title encodes a DNA binding protein.
 #cross-references PMID:91305125
 #accession S16681
 #status preliminary; nucleic acid sequence not shown;
 #molecule_type RNA
 #residues 1-316 #label DEG
 #cross-references EMBL:X56537
 #note the nucleotide sequence was submitted to the EMBL Data
 Library, January 1991
 CLASSIFICATION #superfamily unassigned homeobox proteins; homeobox homology
 KEYWORD DNA binding; homeobox; nucleus; transcription regulation
 FEATURE 73-127
 SUMMARY #domain homeobox homology #label HOX
 #length 316 #molecular_weight 34713 #checksum 3095
 Query Match 1.6%; Score 136; DB 2; Length 316;
 Best Local Similarity 30.9%; Pred. No. 2.4e-03;
 Matches 21; Conservative 20; Mismatches 24; Indels 3; Gaps 3;
 Qy 202 RFWTASSDCSYVRTGIAPRGPAT-SPRPSRSQAQDRSRPARSAPGPAASPGCPGAWTH 260
 Db 261 PARPREQA 268
 Qy 201 RAWNHSHREAGY-PLGLFAPGARRGGSSAISRSLPLPKRPRG-AAPEPERTPVQGGSWAH 258
 Qy 259 PGTRGFS 266

Db 261 PARPREQA 268
 Qy 259 PGTRGFS 266

RESULT 8 A28996 #type complete
 ENTRY proline-rich protein M14 precursor - mouse
 #formal_name Mus musculus #common_name house mouse
 DATE 30-Jun-1999 #sequence_revision 30-Jun-1999 #text_change
 20-Mar-1998
 ACCESSIONS A28996
 REFERENCE Ann, D.K.; Smith, K.; Carlson, D.M.
 #authors J. Biol. Chem. (1988) 263:10887-10893
 #journal Molecular evolution of the mouse proline-rich protein
 multigene family. Insertion of a long interspersed repeated
 DNA element.
 #cross-references PMID:88273214
 #accession A28996
 #molecule_type DNA
 #residues 1-317 #label ANN
 #cross-references GB:M2336; GB:J03891; NID:9200535; PID:g567232
 GENETICS
 #introns 22/1
 CLASSIFICATION #superfamily proline-rich protein
 KEYWORDS saliva
 FEATURE 1-15
 #domain signal sequence #status predicted #label SIG
 16-317
 #product proline-rich protein M14 #status predicted
 #cross-references GB:M2336; GB:J03891
 SUMMARY #length 317 #molecular_weight 31719 #checksum 8454

Query Match 1.6%; Score 132; DB 2; Length 317;
 Best Local Similarity 26.4%; Pred. No. 7.54e-03;
 Matches 39; Conservative 38; Mismatches 64; Indels 7; Gaps 6;

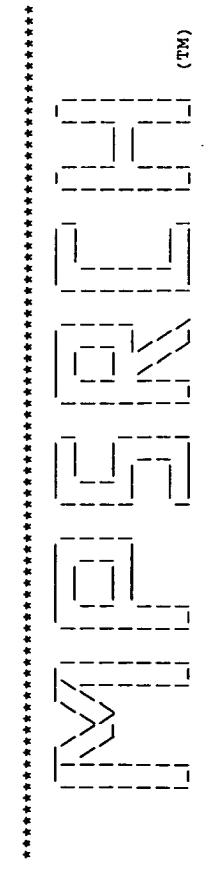
Db 37 SGSQPRPPYNGSQGPPPGPQPRP-PQGPPPPGGPQPRP-QGQPRP-POGP 94
 Qy 180 AAQQARPPHAS--GPERRRLGCB-RANNHSYREAGVYPLGPAGARRGGSARSRLPLK 236
 Db 95 PPGQPRPPQOPPPPG-PQPRPQOPPPPG-PQGPPQGPQPRP-QGQPRPQGPPP 153
 Qy 237 RPRGAAPEPERTPGVGQSWAHPIGRTRGSPSDRGFCVVSPAR-PAAEATSLLEGALSGTRHS 295
 Db 154 GGPPRPGQPPPGPAGPQPRPGQPPP 181
 Qy 296 HPSVGRQHAGPSTSRPRWnTPCPCP 323

RESULT 9 S01955 #type complete
 ENTRY hypothetical protein, 69k - turnip yellow mosaic virus
 TITLE #formal_name turnip yellow mosaic virus, TYMV
 ORGANISM 21-Nov-1993 #sequence_revision 26-May-1995 #text_change
 DATE 26-May-1995
 ACCESSIONS S01955
 REFERENCE March, M.D.; Boyer, J.C.; Haenni, A.L.
 #authors Nucleic Acids Res. (1988) 16:6157-6173
 #journal Overlapping open reading frames revealed by complete
 #title nucleotide sequencing of turnip yellow mosaic virus genomic
 RNA.
 #cross-references MUID:88289359
 #accession S01955
 #status preliminary
 #molecule_type genomic RNA
 #residues 1-628 #label MOR
 #cross-references EMBL:X07441
 #note the authors translated the codon ACG for residue 459 as
 U
 SUMMARY #length 628 #molecular_weight 69194 #checksum 7569
 Query Match 1.6%; Score 137; DB 2; Length 628;
 Best Local Similarity 25.0%; Pred. No. 1.8e-03;
 Matches 73; Conservative 64; Mismatches 134; Indels 21; Gaps 20;

Db 157 GPVLTETKPTSVRQPRPSATRGPSFRILLPKV-VH-VHDDDPHSSLRPGSSRSRQLQPT 214
 Qy 172 GPFLQLGQATQARPPPHAS-GPR-RRLGCEARWNHSYREAGVYPLGPAGAR-RR GGS 227
 Db 215 VRRPLLAQNQFHSPRQPQPLPSDDPGTILGPRLPAPHSTRDPPRPI-TPGPSN-THDLRPL 272
 Qy 228 ASSSLPLKPRPREGAAPPERTVPGVQ-OSWVA-HPGRTRGSPSDRGFCVSPARPAEATSL 285
 Query Match 1.6%; Score 137; DB 2; Length 628;
 Best Local Similarity 25.0%; Pred. No. 1.8e-03;
 Matches 73; Conservative 64; Mismatches 134; Indels 21; Gaps 20;

Db 273 SVLPRTSPRGLLPPNPRRHTSTGHIPPTTSRPTGPPSLRORPVH-LYQSSPHTPNFRP 331
 Qy 286 EG-ALSCTRHSHIPSVGQHAGPPSTSRPRWDTPCPVPPVYAEKHKLY-SSGDKEQLRP 343
 Db 332 SSIRKDAILQTGPRGLHLRQANLRTSERSPPTKRLPSEPNRLPKLPEATLAP 391
 Qy 344 SFLL-SSLR-PSLIGTARRLVETIFGSRPMGPTRPLPLPQWMRPLFELLG- 398
 Db 392 SYRHRRPYPLPNPPAALPSIAYTSSRGKIHSLPKGALPK-EGAPPPLRRL 442
 Qy 399 NHRCQ-CYGVLRKTHCPRA-ATVPAAGVCAKEPQGSVAFAEEEDTDPRRL 448

RESULT 10 S27923 #type complete
 ENTRY gene Lf3 protein - human herpesvirus 4
 TITLE #formal_name human herpesvirus 4, Epstein-Barr virus
 ORGANISM 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
 DATE 08-Sep-1997
 ACCESSIONS S27923
 REFERENCE



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MPsrch_pp

protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 30 14:49:07 1998; MesPar time 50.56 Seconds

942.752 Million cell updates/sec

Title: >US-08-912-951-2

Description: (1-1132) from US08912951.PEP

Perfect Score: 8465

Sequence: 1 MPRAPRRAVRSLLRSHYRE.....TALEAAANPALPSDFKTFILD 1132

Scoring table: PAM 150
Gap 11

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% summaries

Listing first 45 summaries

Database:

sptrembl5
1:sp_fungi 2:sp_invertebrate 3:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_risk 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 53.898; Variance 101.765; scale 0.530

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description Pred. No.

Result No.	Score	Match	Length	DB ID	Description	Pred. No.
1	8465	100.0	1132	2	014746 TELOMERASE REVERSE TRA	0.0e+00
2	8459	99.9	1132	2	014783 TELOMERASE CATALYTIC S	0.0e+00
3	678	8.0	989	1	013339 TELOMERASE REVERSE TRA	6.18e-110
4	681	8.0	989	1	013338 TELOMERASE SUBUNIT P12	1.42e-110
5	439	5.2	1031	3	00939 TELOMERASE CATALYTIC S	3.85e-60
6	439	5.2	1031	3	00939 CHROMOSOME XII COSMID	4.19e-57
7	314	3.7	884	1	006163 PAROTID 'O' PROTEIN (F	2.25e-35
8	142	1.7	234	2	006050 IS 1222 GENE ORF-A AND	3.44e-05
9	141	1.7	276	9	046612 HYPOTHETICAL PROTEIN (4.83e-05
10	147	1.7	296	11	069118 ACTIN ASSOCIATED PROTE	6.21e-06
11	143	1.7	574	13	036027 HOMEBOX PROTEIN (FRAG	2.45e-05
12	136	1.6	316	2	099076 PROLINE RICH PROTEIN P	2.58e-04
13	132	1.6	317	10	062103 SIMILARITY TO COLLAGEN	9.59e-04
14	133	1.6	539	3	02123 HYPOTHETICAL 60.2 KD P	6.92e-04
15	135	1.6	585	11	041935 LF3 PROTEIN	3.59e-04
16	132	1.6	924	11	099307 PROLINE RICH SALIVARY	9.59e-04
17	125	1.5	227	10	HOMOLOGUE OF RETROVIRAL	9.02e-03
18	129	1.5	264	11	PROLINE RICH PROTEIN	2.33e-03
19	131	1.5	300	10	SALIVARY PROLINE-RICH PROTEIN	1.33e-03
20	129	1.5	309	2	Q04118	2.53e-03

ALIGNMENTS

RESULT 1

ID O14746 PRELIMINARY; PRT; 1132 AA.

AC O14746; CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE TELOMERASE REVERSE TRANSCRIPTASE.

GN HPTT.

OS HOMO SAPIENS (HUMAN).

RC TISSUE-KIDNEY; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RA NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H., LINGNER J., HARVEY C.B., CZECH T.R.;

RL SCIENCE 277:955-959 (1997).

DR AF015930; G2330017; EMBL;

KW RNA-DIRECTED DNA POLYMERASE.

SQ SEQUENCE 1132 AA; 126996 MW; 2DFBEDF3 CRC32;

Query Match 100.0%; Score 8465; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0.0e+00;
Matches 1132; Conservative 0; Mismatches 0;
Indices 0; Gaps 0;

Db	1	MPPAPRCAVRSLLRSHYREVPLATEVRLGPGWRLVQRGDPAAFRALVAQCLVCPW 60
Db	1	MPPAPRCAVRSLLRSHYREVPLATEVRLGPGWRLVQRGDPAAFRALVAQCLVCPW 60
Db	61	DARPPPAAPSFROYSCILKEVLVLRQLERICAKRNLYAFGFLALDGARGGPPEAFTSVR 120
Db	61	DARPPPAAPSFROYSCILKEVLVLRQLERICAKRNLYAFGFLALDGARGGPPEAFTSVR 120
Db	121	SILPNTVTDALIGSGANGLLRLLRGGDDVYVHLARCLALFYVAPSCAYQVCGPPIYQLG 180
Db	121	SILPNTVTDALIGSGANGLLRLLRGGDDVYVHLARCLALFYVAPSCAYQVCGPPIYQLG 180
Db	181	ATQARPPPHASGPRRRUGGERAARNHNSVREAGYVPLGLPAPGARRGGSARSLSPLPKPR 240
Db	181	ATQARPPPHASGPRRRUGGERAARNHNSVREAGYVPLGLPAPGARRGGSARSLSPLPKPR 240
Db	241	GAAPEPERTPVQGGSWAHPGRTRGPSPDRGFCTVSPARPAEATSLEGALSGRHSHPSG 300
Db	241	GAAPEPERTPVQGGSWAHPGRTRGPSPDRGFCTVSPARPAEATSLEGALSGRHSHPSG 300
Qy	241	GAAPEPERTPVQGGSWAHPGRTRGPSPDRGFCTVSPARPAEATSLEGALSGRHSHPSG 300

Db	301	ROHHAGPPSTSRRPVRPMDTPCPVVYAEETKHFLLSSGDEQLRPSFLSSLRPSLTGARRL	360	RA	BACCHETTI S., HABER D.A., WEINBERG R.A.;
Qy	301	RQHAGPPSTSRRPVRPMDTPCPVVYAEETKHFLLSSGDEQLRPSFLSSLRPSLTGARRL	360	RL	CELL 90-785-795 (1997);
DR				EMBL; AF018167; G2347129;	
SEQUENCE				1132 AA; 126938 MW; C11E2AF CRC32;	
Query Match			99.9%	Score 8459; DB 2; Length 1132;	
Best Local Similarity			99.9%	Pred. No. 0.01e+00;	
Matches			1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Db	1	MPPAPRCIAVRSLLSRSHREVILPLATEVRLGPQGWLRQGDPAATRALVAQCLVCPW	60		
Qy	1	MPPAPRCIAVRSLLSRSHREVILPLATEVRLGPQGWLRQGDPAATRALVAQCLVCPW	60		
Db	61	DARPPAAPSFRQVSCLKEIYARVLRQICERGAKNVIAFGFALLDARGGPPEAFTTSVR	120		
Qy	61	DARPPAAPSFRQVSCLKEIYARVLRQICERGAKNVIAFGFALLDARGGPPEAFTTSVR	120		
Db	121	SYLPNVTIDALRGSGANGLLLRVGDVYLHLARCALFVLVAPSCAYQVGPPLYQGA	180		
Qy	121	SYLPNVTIDALRGSGANGLLLRVGDVYLHLARCALFVLVAPSCAYQVGPPLYQGA	180		
Db	181	ATQARPPPHASGPGRGGRGASRSPLPKPRR	240		
Qy	181	ATQARPPPHASGPGRGGRGASRSPLPKPRR	240		
Db	241	GAPEPERTYVGQGSWAHPGRGSDRGFCVSPARPAEETSLEGALSGTRHSHPSVG	300		
Qy	241	GAPEPERTYVGQGSWAHPGRGSDRGFCVSPARPAEETSLEGALSGTRHSHPSVG	300		
Db	301	RQHAGPPSTSRRPVRPMDTPCPVVYAEETKFLYSGDKEQLAPSFLSLRPSLTGARRL	360		
Qy	301	RQHAGPPSTSRRPVRPMDTPCPVVYAEETKFLYSGDKEQLAPSFLSLRPSLTGARRL	360		
Db	361	YETIFLGSRPWPGTTPRPLPRIPQRYWMRPLFELIGNHAQCPYGYLTKTCPLRAVT	420		
Qy	361	YETIFLGSRPWPGTTPRPLPRIPQRYWMRPLFELIGNHAQCPYGYLTKTCPLRAVT	420		
Db	421	PAAGVCAREKPQGSVAAPEEEDDPRLRVQLLRQHSSPQWVQGVRCRLRVPGLWG	480		
Qy	421	PAAGVCAREKPQGSVAAPEEEDDPRLRVQLLRQHSSPQWVQGVRCRLRVPGLWG	480		
Db	481	RHNERFLRINTKKFISLGKAHSLSQELTWMNSVRGGCAWLRSRSPGYCVPAAEHRLREEI	540		
Qy	481	RHNERFLRINTKKFISLGKAHSLSQELTWMNSVRGGCAWLRSRSPGYCVPAAEHRLREEI	540		
Db	541	LAKFLHNTMSYYVELLRSFFYETETFQKNRLFFYFKSWSKLSQISGIRQLKRYOLRE	600		
Qy	541	LAKFLHNTMSYYVELLRSFFYETETFQKNRLFFYFKSWSKLSQISGIRQLKRYOLRE	600		
Db	601	LSBAEVROHREARPALLTSRLRIPKPDGLRPVNMDDYVVGARTFREKRAERLTSVKA	660		
Qy	601	LSBAEVROHREARPALLTSRLRIPKPDGLRPVNMDDYVVGARTFREKRAERLTSVKA	660		
Db	651	LFSVLNTYERREGPLGASVLGLDDIHRAWRFTFVLRQAQDPPELYFVKVDVTGAYDTI	720		
Qy	661	LFSVLNTYERREGPLGASVLGLDDIHRAWRFTFVLRQAQDPPELYFVKVDVTGAYDTI	720		
Db	721	PODLTEVYASTIKPONTYCYRYAVQKAAGHVYKAKFHSVSTLTLQPMRQFYAHL	780		
Qy	721	PODLTEVYASTIKPONTYCYRYAVQKAAGHVYKAKFHSVSTLTLQPMRQFYAHL	780		
Db	841	LCSLCYGDMENTKLAGIRRDGULLRLVDFLTMCHHAIRCKSYTQCQGTFQGSTLSTL	840		
Qy	781	QETSPRDAVYEQSSLINEASGLFDYFLRMCHHAIRCKSYTQCQGTFQGSTLSTL	840		
Db	841	LCSLCYGDMENTKLAGIRRDGULLRLVDFLTMCHHAIRCKSYTQCQGTFQGSTLSTL	840		
Qy	841	QETSPRDAVYEQSSLINEASGLFDYFLRMCHHAIRCKSYTQCQGTFQGSTLSTL	840		
Db	901	RKTVVNPVEDEAQGTAFVQMPAHGLFWCQLLDPTRTLEYQSDYSSYARTSIRASLTF	960		
Qy	901	RKTVVNPVEDEAQGTAFVQMPAHGLFWCQLLDPTRTLEYQSDYSSYARTSIRASLTF	960		
Db	961	NRGFKAGRNMKRLFGTYLRLICHSLFDLQLNSLOCTCNITKILLQAYREHACVYQLP	1020		
Qy	961	NRGFKAGRNMKRLFGTYLRLICHSLFDLQLNSLOCTCNITKILLQAYREHACVYQLP	1020		
Db	1021	FHQQVNKNPTEFLRVLISDTASLICYSILKAKNAGMSLGAKGAGGPLSEAVQMLCHQAFL	1080		
Qy	1021	FHQQVNKNPTEFLRVLISDTASLICYSILKAKNAGMSLGAKGAGGPLSEAVQMLCHQAFL	1080		
Db	1081	KLTRRHRTYVPLGSLATAQTOSLRKLPGTTLTALEAANPALSDEFTILD	1132		
Qy	1081	KLTRRHRTYVPLGSLATAQTOSLRKLPGTTLTALEAANPALSDEFTILD	1132		
Db	1081	OS HOMO SAPiens (HUMAN).			
OC	1081	EUKARYOTIA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	1081	EUTHROPHIA; PRIMATES.			
RN	[1]	RESULT 2 PRELIMINARY; PRT: 1132 AA.			
ID	014783				
AC	014783;				
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)				
DE	TELOMERASE CATALYTIC SUBUNIT.				
GN	NEST2.				
OS	HOMO SAPiens (HUMAN).				
OC	EUKARYOTIA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
RN	[1]	SEQUENCE FROM N.A.			
RP	MEYERSON M., COUNTER C.M., EATON E.N., ELLISEN L.W., STEINER P.,				
RA	CAZZOLE S.D., ZIAUGRA L., BEIJERSBERGEN R.L., DAVIDOFF M.J., LIU Q.,				
RA	RKTIVNNPVEDEALGGTAFVQMPAHGLFWCQLLDPTRTLEYQSDYSSYARTSIRASLTF	960			
RA	RKTIVNNPVEDEALGGTAFVQMPAHGLFWCQLLDPTRTLEYQSDYSSYARTSIRASLTF	960			

Db	961	NRGFKAGRNMRKLFGLVRLKHSFLDQVNSLQTYCTNIKILLQAYRFHACVLQLP	1020
Qy	961	NRGFKAGRNMRKLFGLVRLKHSFLDQVNSLQTYCTNIKILLQAYRFHACVLQLP	1020
Db	1021	FHQQWKNPTEFLRVISDTASLCYSLAKNAGMSLAGKAAGPLPSEAVQWLQHAQFLL	1080
Qy	1021	FHQQWKNPTEFLRVISDTASLCYSLAKNAGMSLAGKAAGPLPSEAVQWLQHAQFLL	1080
Db	1081	KLTRHRVTTYPLLGSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTILD	1132
Qy	1081	KLTRHRVTTYPLLGSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTILD	1132
RESULT	3	PRELIMINARY;	PRT; 988 AA.
ID	O13319		
AC	O13319;		
DT	01-JAN-1998	(TREMBLER, 05, CREATED)	
DT	01-JAN-1998	(TREMBLER, 05, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998	(TREMBLER, 05, LAST ANNOTATION UPDATE)	
DE	TELOMERASE REVERSE TRANSCRIPTASE 1.		
DE	TRET1.		
KW	SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)		
KW	EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=97RH;		
RA	NAKAMURA T. M., MORIN G. B., CHAPMAN K. B., WEINRICH S. L., ANDREWS W. H.,		
RA	LINGNER J., HARLEY C. B., CECH T. R.;		
RA	SCIENCE 277: 955-959(1997).		
DR	EMBL: AF015783; G2340168; -.		
DR	RNA-DIRECTED DNA POLYMERASE.		
SQ	SEQUENCE 988 AA; 116328 MW; 39C305A7 CRC32;		
		8.0% Score 678; DB 1; Length 988;	
Query	Match	Best Local Similarity 26.4%; Pred. No. 6.18e-110;	
Matches	129;	Conservative 133; Mismatches 208; Indels 18; Gaps 15	
Db	340	PNOQFAFLRSVFLRVPPFLNGQRPIFEILKDLTEFLKLSRYESFSFLHYLMNSNIKISEI	399
Qy	458	FWQYGFVRACLRFLPGLMGRHNRRFLANTKKFISLGKHAKHQLWTMYSRVRDC	517
Db	400	EWIVLGKRSNAKMCISPEKKR_KQ_IFAEFLWLYNSLIPILQSFYIETESSDILRNVTV	457
Qy	518	AWL--_RSRSPGVCGVCPAERHLREELIAKEFLWLMSTVVYELLRSRFVYTETFFQKNRLF	574
Db	458	YFRKDITW-KLLCRPFTTSKMKBAFEKINENNYVRMDTQ_KTTLBPAVIRLLPKNTFRFLIT	515
Qy	575	FYRKWSKLASKIGIROHLKVKOLRESAEYRQHREPRALLTSRKRFLPKDGLRPFV	634
Db	516	NLRKRELIKMGNSNNKMLVNSTNOLRPAVSLKHLINFESSGIPFN-LEVYMKLITEKKDL	574
Qy	635	NMDYVVGARTFRREKARLTSRVAKFSLVAYERARPLGQVSGLSDDIHRAWTRWE	694
Db	575	LKHMFRGRK_K-YFVFRDIKSCYDRIODLMRIVKKLKKDPE_FVIRKYATH-ATSDR	630
Qy	695	LRVRAQDPPPELYFWVDTGAYDTIQDRLTEVIASLIKPONTYCYARRAYQKAAGH	754
Db	631	ATKNPVSEAFSYFDMYFEK --VVQLLSMKTT-SDTLFDYDWTWIKSSSEIFKMLKEHLS	687
Qy	755	VRKAKSHVSVLTDQYMRQTVHLGETSPREDAVIYEQSSSINEASGLGDYFLRFRFC	814
Db	688	GHTVKIGNSQYLQKVGSQPOGSTLSSFLCHFYMEDLIDEYLSTFKKKGSVLLRYVDDELFI	747
Qy	815	HHAVTRGKSIVQVCGQPGQSLSLTCYGDMEKRLFGTRRDG-LLRLYLVDFLLV	873
Db	748	TWNKDKAKKFNLSLRQEPEKHFNSTSLEKTVINFENGSLINTTFFNSKKR_M-PFFFEE	805
Qy	874	TPLHJTHAKTEFLRTLVRCGYPEGCVVNLRKTVVNFPEVDEALGTAFTVQMPAHGLFPWCGL	933
Db	806	SVNMRSLID 813	
Qy	934	LDDTRILE 941	

Matches 45; Conservative 31; Mismatches 54; Indels 12; Gaps 11;

Db 315 AGSPPPPPRGSPTGSLPPQA-GGSPPPACT-GSPPPQQKQAPERSSPP-TGSP 370
 Qy 179 GATQARPYPHASPPRRLGCEAQNHSVREAGYPLGLPAPGARRGSEASRSPLPKRP 238

Db 371 PTGSPP-TGRPPRGPGKSSEESSESREGPRGGPRGGPKSSEESSESSEPRGPR 429
 Qy 239 RRGAAPEERTP-YGOG-SWAHGRTR-GP-SU-RGFCVVSPARPAEATSLLEGALSGTR 293

Db 430 RSPPT-GSPP-TGSPTGRRPR 449
 Qy 294 HSPSVGRQHAGPPSTSRRPR 315

RESULT 15 PRELIMINARY; PRT: 585 AA.

ID 041935; AC 041935; DT 01-JAN-1998 (TREMELREL. 05, CREATED)
 DT 01-JAN-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)

CN HYPOTHETICAL 60.2 KD PROTEIN.
 GAMMAHV M6.

OS MORINE HERPESVIRUS 68.

QC DS DNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE; GAMMAHERPESVIRNAE.

RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=NUMS;
 RC MEDLINE: 97366649
 RA VIRGIN H.W. IV, LATREILLE P., WANSLEY P., HALLSWORTH K., WECK K.E.,
 DAL CANTO A.J., SPECK S.H.;
 RL J. VIROL. 71:5894-5904(1997).
 RN [2]
 RP STRAIN=NUMS;
 RC LATREILLE P., WANSLEY P., WATERSTON R.H.;
 RL SUBMITTED TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U97553; G2317934; -.
 KW HYPOTHETICAL PROTEIN.

SQ SEQUENCE 585 AA; 60160 MN: B35C72E5 CRC32;

Query Match 1.6%; Score 135; DB 11; Length 585;
 Best Local Similarity 27.6%; Pred. No. 3.59e-04;
 Matches 45; Conservative 37; Mismatches 68; Indels 13; Gaps 11;

Db 342 PPE-ELGGSPTPSAPSARGARPDPLPSGSPDPPRPPPELGSPTPAPSAG 400
 Qy 173 PPLYOLGATAQAPPHASGPRR-L-CGERANNHSVREA-GVP-LGLPAPGARRGGSA 228

401 ARTDPLGPPLPSNGPDPRPRPPPELGP-GSPPT-SPASRAGARIPRSRPBDLGP-G 456
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 229 SRSLPLPKR-PRGAAPPERTVGQGSWAHPCTRGPDSRGCVSPARPAEATSLLEG 287

457 SPFRPRPRP-PELGGSPTDGPPLPSWG-PDPPTPAPSR 496
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 288 ALSGTRISHPSVGRQHAGPPSTSRRPRBWDTCPPVIAETKH 330

Search completed: Thu Jul 30 14:51:34 1998
 Job time : 147 secs.